Figure 1

SEQ ID NO:1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV   60

VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG   120

ADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF   180

LNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC   227

SEQ ID NO:2

DEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFP   60

GAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPP   120

AHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQD   180

SPTLQAPRERASEPKHKNQAEIAAC   205

SEQ ID NO:3

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV   60

VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG   120

ADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF   180

LNRFHLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRRR   223

SEQ ID NO:4

DEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFP   60

GAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPP   120

AHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQD   180

SPTLQAPRGRASEPKHKTRRR   201

SEQ ID NO:5

ITSWMEPIVK   10

SEQ ID NO:6

FPGAVDGATYILVMVDPDAPSR   22

SEQ ID NO:7

HWLVTDIK   8

SEQ ID NO:8

IQGQELSAYQAPSPPAHSGFHR   22

SEQ ID NO:9

YQFFVYLQEGK   11

SEQ ID NO:10

VISLLPK   7

Figure 2

CLUSTAL W (1.81) multiple sequence alignment

```
PEBP_HUMAN    ------PVDLSKWSGPLSLQEVDEQPQHP-------------------LHVTYAGAAVDELGK
PEBP_BOVIN    ------PVDLSKWSGPLSLQEVDERPQHP-------------------LQVKYGGAEVDELGK
Q96S96        MGWTMRLVTAALLGLMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYP--ELGNIGC
                   *    **  ::  :  *          *    *  :::  * ::::*

PEBP_HUMAN    VLTPTQVKNRPTSISWDG--------LDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNM
PEBP_BOVIN    VLTPTQVKNRPTSITWDG--------LDPGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNM
Q96S96        KVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDI
               : .  :   .    *    .:      *  ****  ********* :*:   *  *:*:*:*  :::

PEBP_HUMAN    KGNDISSG----TVLSDYVGSGPPKGTGLHRYVWLVYEQDRPLKCDEPILSNRSGDHRGK
PEBP_BOVIN    KGNNISSG----TVLSDYVGSGPPKGTGLHRYVWLVYEQEGPLKCDEPILSNRSGDHRGK
Q96S96        KGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVIS----LLPKENKTRGS
              **  :      * ****  :*::** :::*** : :**:** :  .  : :**

PEBP_HUMAN    FKVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSGK--------------
PEBP_BOVIN    FKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSGK--------------
Q96S96        WKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC
              :*:  * :::: ::   : *   .  **    *  *
```

Figure 3

CLUSTAL W (1.81) multiple sequence alignment

```
Q9D9G2   --MTMKLVAAALCLRLLAAGLWVGLSLTAESIEEGKPGGEKPGGGKPGGSGRGCFLPPLP
Q9D9L9   --MTMKLVAAALCLSLLAAGLWVGLSLTAESIEEGKPGGEKPGGGKPGGSGRGCFLPPLP
Q96S96   MGWTMRLVTAALLLGLMMV------VTGD-EDENSP-------------CAHEALL
Q8WW74   MGWTMRLVTAALLLGLMMV------VTGD-EDENSP-------------CAHEALL
            * :.* *:  .* :**  * ..*                   *  .  *

Q9D9G2   KEDVSLCRNLEVFYMEMGNISCKIVPKCNLYRQKIPAWQAPIVKFHTALDGALYLLVMVD
Q9D9L9   KEDVSLCRNLEVFYMEMGNISCKIVPKCNLYRQKITAWQAPIVKFHTALD---------
Q96S96   DEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVD
Q8WW74   DEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVD
          .** :.* ***** * ***.**:**.** ****:.:*      ****    * ****** *

Q9D9G2   PDAPSRSNPVMKYWRHWLVSNITGADMKSGSIRGNVLSDYSPPTPPPETGVHRYQFFVYL
Q9D9L9   ------------------VS-----ELGWLKENVGP-----------------
Q96S96   PDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYL
Q8WW74   PDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYL
          ******            *  ***     * ***          *         *********

Q9D9G2   QGDRDISLSVEEKANLGGWNLDKFLQQYGLRDPDTSTQFMTQFDEELSSEFGRINDDQEQ
Q9D9L9   ------------------------------------
Q96S96   QEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEP
Q8WW74   QEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRGRASEP
          *   *** *  ***   * ***    **       ***      *  ********

Q9D9G2   FNQK-------
Q9D9L9   -----------
Q96S96   KHKNQAEIAAC
Q8WW74   KHKTRRR----
             *
```

Figure 4